

#10

1653

Ram  
 RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/518,297

DATE: 08/15/2001  
 TIME: 12:28:02

Input Set : A:\4600-0130.30-SEQLIST.TXT  
 Output Set: N:\CRF3\08152001\I518297.raw

4 <110> APPLICANT: Lim, Moon Young  
 5 Edwards, Cynthia A.  
 6 Fry, Kirk E.  
 7 Bruice, Thomas W.  
 8 Starr, Douglas B.  
 9 Laurance, Megan E.  
 10 Kwok, Yan  
 13 <120> TITLE OF INVENTION: DNA Binding Compound-Mediated Molecular  
 14 Switch System  
 16 <130> FILE REFERENCE: 4600-0130.30  
 18 <140> CURRENT APPLICATION NUMBER: US 09/518,297  
 19 <141> CURRENT FILING DATE: 2000-03-03  
 21 <150> PRIOR APPLICATION NUMBER: US 60/122,513  
 22 <151> PRIOR FILING DATE: 1999-03-03  
 24 <150> PRIOR APPLICATION NUMBER: US 60/154,605  
 25 <151> PRIOR FILING DATE: 1999-09-17  
 27 <160> NUMBER OF SEQ ID NOS: 62  
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 11  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Artificial Sequence  
 36 <220> FEATURE:  
 37 <223> OTHER INFORMATION: DNA response element  
 39 <400> SEQUENCE: 1  
 40 cgttcgcact t 11  
 42 <210> SEQ ID NO: 2  
 43 <211> LENGTH: 17  
 44 <212> TYPE: DNA  
 45 <213> ORGANISM: Artificial Sequence  
 47 <220> FEATURE:  
 48 <223> OTHER INFORMATION: DNA response element  
 50 <400> SEQUENCE: 2  
 51 cggagtactg tcctccg 17  
 53 <210> SEQ ID NO: 3  
 54 <211> LENGTH: 12  
 55 <212> TYPE: DNA  
 56 <213> ORGANISM: Artificial Sequence  
 58 <220> FEATURE:  
 59 <223> OTHER INFORMATION: DNA response element  
 61 <221> NAME/KEY: misc\_feature  
 62 <222> LOCATION: (1)...(12)  
 63 <223> OTHER INFORMATION: n = A,T,C or G  
 65 <400> SEQUENCE: 3  
 66 taattanggg ng 12  
 68 <210> SEQ ID NO: 4  
 69 <211> LENGTH: 551

ENTERED

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70 <212> TYPE: PRT  
71 <213> ORGANISM: Homo sapiens  
73 <220> FEATURE:  
74 <221> NAME/KEY: VARIANT  
75 <222> LOCATION: (0)...(0)  
76 <223> OTHER INFORMATION: transcriptional regulatory protein  
78 <400> SEQUENCE: 4  
79 Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala  
80 1 5 10 15  
81 Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met  
82 20 25 30  
83 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly  
84 35 40 45  
85 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn  
86 50 55 60  
87 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp  
88 65 70 75 80  
89 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg  
90 85 90 95  
91 Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser  
92 100 105 110  
93 Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln  
94 115 120 125  
95 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro  
96 130 135 140  
97 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys  
98 145 150 155 160  
99 Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro  
100 165 170 175  
101 Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala  
102 180 185 190  
103 Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly  
104 195 200 205  
105 Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile  
106 210 215 220  
107 Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser  
108 225 230 235 240  
109 Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro  
110 245 250 255  
111 Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu  
112 260 265 270  
113 Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr  
114 275 280 285  
115 Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg  
116 290 295 300  
117 Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly  
118 305 310 315 320  
119 Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg  
120 325 330 335

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121 Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr  
122 340 345 350  
123 Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe  
124 355 360 365  
125 Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro  
126 370 375 380  
127 Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val  
128 385 390 395 400  
129 Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly  
130 405 410 415  
131 Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly  
132 420 425 430  
133 Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu  
134 435 440 445  
135 Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr  
136 450 455 460  
137 Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln  
138 465 470 475 480  
139 Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr  
140 485 490 495  
141 Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp  
142 500 505 510  
143 Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu  
144 515 520 525  
145 Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala  
146 530 535 540  
147 Leu Leu Ser Gln Ile Ser Ser  
148 545 550  
150 <210> SEQ ID NO: 5  
151 <211> LENGTH: 19  
152 <212> TYPE: DNA  
153 <213> ORGANISM: Artificial Sequence  
155 <220> FEATURE:  
156 <223> OTHER INFORMATION: DNA response element  
158 <400> SEQUENCE: 5  
159 tccctatcaag tgatagaga 19  
161 <210> SEQ ID NO: 6  
162 <211> LENGTH: 22  
163 <212> TYPE: DNA  
164 <213> ORGANISM: Artificial Sequence  
166 <220> FEATURE:  
167 <223> OTHER INFORMATION: response element  
169 <400> SEQUENCE: 6  
170 cttAACACTC gcgagggtta ag 22  
172 <210> SEQ ID NO: 7  
173 <211> LENGTH: 13  
174 <212> TYPE: DNA  
175 <213> ORGANISM: Artificial Sequence  
177 <220> FEATURE:

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178 <223> OTHER INFORMATION: response element  
 180 <221> NAME/KEY: misc\_feature  
 181 <222> LOCATION: (3)...(3)  
 182 <223> OTHER INFORMATION: n = G or T  
 184 <221> NAME/KEY: misc\_feature  
 185 <222> LOCATION: (7)...(7)  
 186 <223> OTHER INFORMATION: n = A,T,C or G  
 188 <221> NAME/KEY: misc\_feature  
 189 <222> LOCATION: (12)...(12)  
 190 <223> OTHER INFORMATION: n = A or C  
 192 <400> SEQUENCE: 7  
 193 rgmtcantga cny 13  
 195 <210> SEQ ID NO: 8  
 196 <211> LENGTH: 77  
 197 <212> TYPE: PRT  
 198 <213> ORGANISM: Artificial Sequence  
 200 <220> FEATURE:  
 201 <223> OTHER INFORMATION: activator sequence  
 203 <400> SEQUENCE: 8  
 204 Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly  
 205 1 5 10 15  
 206 Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu  
 207 20 25 30  
 208 Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His  
 209 35 40 45  
 210 Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu  
 211 50 55 60  
 212 Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly  
 213 65 70 75  
 215 <210> SEQ ID NO: 9  
 216 <211> LENGTH: 11  
 217 <212> TYPE: PRT  
 218 <213> ORGANISM: Artificial Sequence  
 220 <220> FEATURE:  
 221 <223> OTHER INFORMATION: activator sequence  
 223 <221> NAME/KEY: VARIANT  
 224 <222> LOCATION: (1)...(11)  
 225 <223> OTHER INFORMATION: tetramer  
 227 <400> SEQUENCE: 9  
 228 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu  
 229 1 5 10  
 231 <210> SEQ ID NO: 10  
 232 <211> LENGTH: 97  
 233 <212> TYPE: PRT  
 234 <213> ORGANISM: Artificial Sequence  
 236 <220> FEATURE:  
 237 <223> OTHER INFORMATION: repressor sequence  
 239 <400> SEQUENCE: 10  
 240 Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe

## RAW SEQUENCE LISTING

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Input Set : A:\4600-0130.30-SEQLIST.TXT  
 Output Set: N:\CRF3\08152001\I518297.raw

```

241 1           5           10           15
242 Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
243           20           25           30
244 Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
245           35           40           45
246 Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
247           50           55           60
248 Arg Leu Glu Lys Gly Glu Pro Trp Leu Val Glu Arg Glu Ile His
249 65           70           75           80
250 Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
251           85           90           95
252 Val
255 <210> SEQ ID NO: 11
256 <211> LENGTH: 36
257 <212> TYPE: PRT
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: repressor sequence
263 <400> SEQUENCE: 11
264 Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
265 1           5           10           15
266 Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
267           20           25           30
268 Met Leu Pro Tyr
269           35
271 <210> SEQ ID NO: 12
272 <211> LENGTH: 116
273 <212> TYPE: DNA
274 <213> ORGANISM: Escherichia coli
276 <220> FEATURE:
277 <221> NAME/KEY: misc_feature
278 <222> LOCATION: (0)...(0)
279 <223> OTHER INFORMATION: partial promoter sequence
281 <400> SEQUENCE: 12
282 cgcggtcaga aaatttatttt aaatttcctc ttgtcaggcc ggaataactc cctataatgc      60
283 gccaccactg acacgaaaca acggcaaaca cggcccccggg tcagcgggt ttcct      116
285 <210> SEQ ID NO: 13
286 <211> LENGTH: 22
287 <212> TYPE: DNA
288 <213> ORGANISM: Escherichia coli
290 <220> FEATURE:
291 <221> NAME/KEY: misc_feature
292 <222> LOCATION: (0)...(0)
293 <223> OTHER INFORMATION: partial promoter sequence
295 <400> SEQUENCE: 13
296 agaaaattat tttaaatttc ct      22
298 <210> SEQ ID NO: 14
299 <211> LENGTH: 22
300 <212> TYPE: DNA

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/518,297

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Input Set : A:\4600-0130.30-SEQLIST.TXT  
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L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7